Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
Filing Date: September 12, 2003
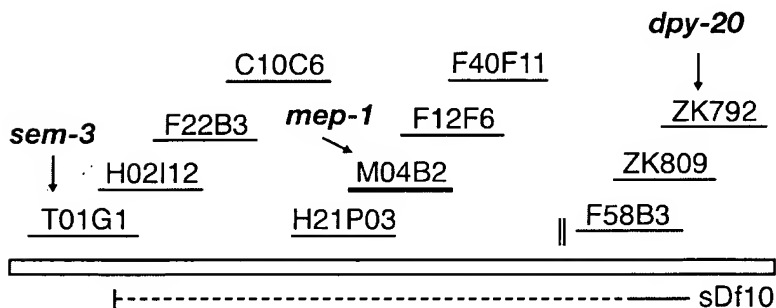Serial No. 10/661,398
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Fig. 1A

```
                            C10C6              F40F11                 dpy-20
                                                                        ↓
       sem-3     F22B3      mep-1   F12F6                             ZK792
         ↓  · H02I12          ↘                            ZK809
       T01G1                 M04B2
                   H21P03                       ‖  F58B3
```



```
sDf10
```

```
M V T A D E T V L A T T T N T T S M S V E P T D P R S A G E   30

S S S D S E P D T I E Q L K A E Q R E V M A D A A N G S E V   60

N G N Q E N G K E E A A S A D V E V I E I D D T E E S T D P   90

S P D G S D E N G D A A S T S V P I E E E A R K K D E G A S   120

E V T V A S S E I E Q D D D G D V M E I T E E P N G K S E D   130

T A N G T V T E E V L D E E E P E P S V N G T T E I A T E K   180

E P E D S S M P V E Q N G K G V K R P V E C I E L D D D D D   210

D E I Q E I S T P A P A K K A K I D D V K A T S V P E E D N   240

N E Q A Q K R L L D K L E E Y V K E Q K D Q P S S K S R K V   270

L D T L L G A I N A Q V Q K E P L S V R K L I L D K V L V L   300
                  ▾ n3680 S309N
P N T I S F P P S Q V C D L L I E H D P E M P L T K V I N R   330

M F G E E R P K L S D S E K R E R A Q L K Q H N P V P N M T   360

K L L V D I G Q D L V Q E A T Y C D I V H A K N L P E V P K   390

N L E T Y K Q V A A Q L K P V W E T L K R K N E P Y K L K M   420

H R C D V C G F Q T E S K L V M S T H K E N L H F T G S K F   450
                                          ▾ n3703 splice
Q C T M C K E T D T S E Q R M K D H Y F E T H L V I A K S E   480

E K E S K Y P C A I C E E D F N F K G V R E Q H Y K Q C K K   510

D Y I R I R N I M M P K Q D D H L Y I N R W L W E R P Q L D   540

P S I L Q Q Q Q Q A A L Q Q A Q Q K K Q Q Q L L H Q Q Q A A   570

Q A A A A Q L L R K Q Q L Q Q Q Q Q Q Q A R L R E Q Q Q   600

A A Q F R Q V A Q L L Q Q Q S A Q A Q R A Q Q N Q G N V N H   630

N T L I A A M Q A S L R R G G Q Q G N S L A V S Q L L Q K Q   660

M A A L K S Q Q G A Q Q L Q A A V N S M R S Q N S Q K T P T   690
                               ▾ n3702 Q706 amber
H R T P T F V C E I C D A S V Q E K E K Y L Q H L Q T T H K   720

Q M V G K V L Q D M S Q G A P L A C S R C R D R F W T Y E G   750

L E R H L V M S H G L V T A D L L L K A Q K K E D G G R C K   780

T C G K N Y A F N M L Q H L V A D H Q V K L C S A E I M Y S   810

C D V C A F K C S S Y Q T L E A H L T S N H P K G D K K T S   840

T P A K K D D C I T L D D                                     853
```

Fig. 1B

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mep-1 genomic sequence

TCACACACTCATGACATACACACATCATTTCGCCTCACACACCGCGCCGTCGCCATCCGCACCG
CCCGGGTGGGACGTGTTCAAACTTTTCGGTTTTCGTAATTAATAGTGAGCCCCGGTTTATTCGC
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ATTAACTGTTTTAAATTTATCTGCCTTTATCGTTACAGTAAATCATTTTGATGAACTTTTCGGA
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TGCCCGGCTTATTTTTGGTGATTGAAGCATGATTCTGTTGACGCTCCCGACGCGGAATACCAG
GACGGACCGATGAGAGAGTACTGCCAGTGAAGAGACGCATGCGAGCAGGACGAGTGCTGCTCAC
CCTTCTTCTCAGCGTCGGCGGCTGCGACCAGCGGCCGAGGAAGGGGAGGAGAGAGGCCGATTTG
GCTGCGTACCACGTTTGATACTCAGTCACTTACCACAGCTGGTTCTCTTGTGCGTTCAAATCTG
GCTTGCCGCGCGCGCATTTTATTCCTACCAGTTTGAATCTCCCACCTCTCCGACTGTAACTG
TCCTAATTTGCTTCCTTCTCATCACTCTCTCTTTGCCTATTTCTCACTATCTAGACTCTATTTT
TCCAGA ATG GTCACCGCCGACGAGACGGTACTCGCCACAACGACCAACACCACTTCCATGTCTG
TGGAACCAACGGATCCGAGAAGCGCTGGTGAATCGTCCTCAGATTCGGAGCCAGACACAATTGA
GGTGAGGAAAAGTTTTGGGAATTTAAATCTGAATAAAACGTTTTCAGCAGCTGAAGGCAGAACA
GCGCGAAGTGATGGCCGACGCGGCGAATGGTTCCGAAGTCAACGGAAATCAAGAGAACGGAAAA
GAGGAAGCGGCATCTGCAGACGTGGAAGTGATCGAGATAGATGACACCGAAGAGTCTACGGATC
CCTCACCTGATGGATCTGATGAAAACGGTGATGCTGCATCTACATCGGTTCCAATCGAAGAGGA
AGCGCGTAAAAAGGATGAGGGGGCTTCCGAAGTGACTGTGGCATCATCTGAGATTGAACAAGAC
GATGATGGCGATGTTATGGAAATCACTGAGGAGCCGAACGGAAAGTCGGAGGATACTGCCAACG
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CGGACACGAGTGAGCAAAGAATGAAGGATCACTACTTGTAAGTTTTTTTTTTTCATCTTTCAA
TATTCATTTAATTACAGCGAAACTCATCTTGTTATTGCAAAATCGGAAGAGAAGGAGTCCAAGT
ATCCATGTGCAATCTGCGAAGAAGACTTCAATTTCAAAGGTGTCCGTGAGCAGCATTACAAGCA
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CTGCTCTTCAGCAAGCTCAACAAAAGAAGCAACAGCAACTTCTGCATCAACAGCAAGCAGCACA
AGCTGCAGCCGCTGCGCAACTCTTACGGAAGCAACAATTACAACAGCAACAACAACAGCAACAG

Fig. 2A

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GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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GCTCGTCTTCGTGAGCAACAGCAAGCGGCCCAATTCCGGCAAGTGGCTCAACTGCTGCAACAAC
AATCAGCGCAGGCTCAACGTGCACAGCAGAATCAAGGAAATGTGAATCATAACACTCTGATTGC
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AGATCAGTATACACTTTCACTTCATACGTCTGTTGTTCTCCCCCATCTCATACTTTTTTTACCA
TTTGTCCAGTTAAGATTTTTGGAAGATATCTAT

Fig. 2B

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mep-1 ORF

```
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TGTCTGTGGAACCAACGGATCCGAGAAGCGCTGGTGAATCGTCCTCAGATTC
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AAGCGGCATCTGCAGACGTGGAAGTGATCGAGATAGATGACACCGAAGAGTC
TACGGATCCCTCACCTGATGGATCTGATGAAACGGTGATGCTGCATCTACA
TCGGTTCCAATCGAAGAGGAAGCGCGTAAAAAGGATGAGGGGGCTTCCGAAG
TGACTGTGGCATCATCTGAGATTGAACAAGACGATGATGGCGATGTTATGGA
AATCACTGAGGAGCCGAACGGAAAGTCGGAGGATACTGCCAACGGAACAGTT
ACTGAGGAGGTGCTAGATGAAGAGGAGCCAGAACCTTCCGTAAACGGAACAA
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GATGATGACGAGATTCAGGAAATTTCTACCCCTGCCCCAGCTAAAAAAGCTA
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GGCGCAGAAGAGATTGCTCGACAAGCTGGAAGAGTATGTGAAGGAGCAGAAG
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TCAATGCGCAAGTTCAAAAGGAGCCTCTGTCGGTTCGGAAGCTGATCCTGGA
CAAAGTTCTCGTTCTCCCAAACACAATATCATTCCCACCAAGTCAAGTTTGC
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CCGAAGCAAGACGATCATCTCTATATCAACAGATGGCTCTGGGAGAGGCCCC
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GCAGCCGCTGCGCAACTCTTACGGAAGCAACAATTACAACAGCAACAACAAC
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GGCTCAACTGCTGCAACAACAATCAGCGCAGGCTCAACGTGCACAGCAGAAT
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GTAGAGGTGGTCAACAAGGAAATTCGCTGGCAGTTTCTCAACTTCTCCAAAA
GCAAATGGCAGCTTTGAAGTCGCAACAAGGAGCTCAACAACTTCAGGCTGCG
GTGAACTCCATGAGAAGCCAGAACAGTCAAAAGACGCCAACACACAGAACTC
```

Fig. 3A

Title: RB PATHWAY AND CHROMATIN REMODELING
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CCACGTTTGTATGCGAAATTTGTGATGCGTCAGTGCAGGAAAAGGAGAAGT
ATCTACAGCATCTTCAGACTACTCATAAGCAGATGGTTGGAAAAGTGCTGC
AGGACATGTCGCAAGGAGCTCCACTGGCATGTTCTCGATGCCGTGACAGAT
TCTGGACTTATGAAGGGTTGGAGCGGCACTTGGTGATGTCGCATGGTCTCG
TCACTGCTGATCTGCTCCTCAAAGCGCAAAAGAAGGAAGACGGAGGTCGAT
GCAAGACATGCGGCAAGAACTATGCGTTCAACATGCTTCAACACTTGGTAG
CTGATCATCAAGTGAAGTTGTGCTCGGCTGAAATCATGTACTCGTGCGATG
TGTGCGCGTTCAAATGCTCGAGTTATCAGACTCTGGAAGCCCATCTCACTT
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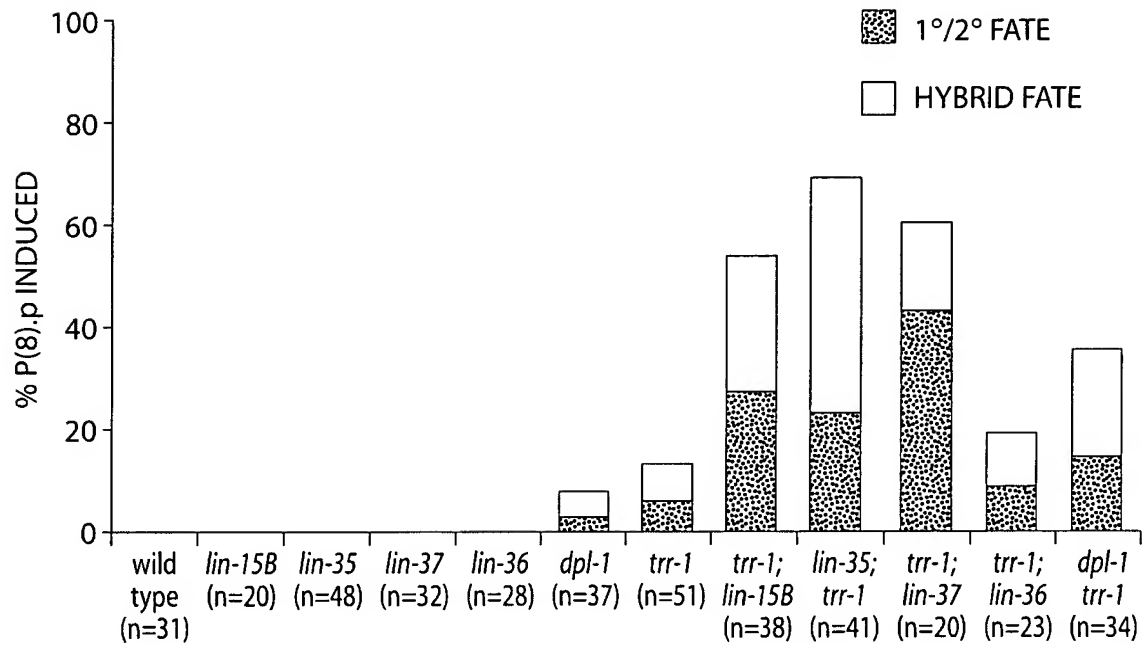ATTGTATTACTCTGGATGATTAA

Fig. 3B

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
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Fig. 6

Title: RB PATHWAY AND CHROMATIN REMODELING
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ssl-1 Genomic
```
cagctgatgt tgttgatgga aaaatgacgg ctgcaaagaa gccattggct gcaactgagc  60
caaaagtgca taataaataa atgtgtttct aggatcttct aataattttt tttctgtttt  120
ctagctctaa acttgtattt atttcattct tgttctacca aattcccacg gattctacgc  180
tttatgtttc taaattatta ttctttttta tttatatctg cattttcttc taaaaactct  240
ggtcatttc ttgttttttt cttggtaatt ataaaaatta gtcatacaaa tcttgttaaa  300
tatctggcta ttcagtgaac aaaccatttt ccgctctaaa ttcgacccga atcaatcgaa  360
aaatggctca aaacgatgcc atctggctgc aaccccctg tcgtctctca attttgtgta  420
ctctctcgca gccacgcacg cgacgcaacg cactcgcgtc gcggtcgcag ttctttttca  480
aatttatcgc gccattttg ttttgcctca tatttatcgg ctcacgattg attttcgtcg  540
aaaaacgcgc ttaatcgatt ccttttacc tgaaaaatgt tgttccaatt ggaaaaccag  600
ttgaagatcg atgaattttc aagaaaatca ttcaaatagg caaaacccgc tgaactttga  660
aattcgattt ttgagttttt tgaagaaaat ataattattt catcatttat gttggtcctg  720
ttggtcctca gcatagaaaa ttcggacatg acattagaaa ttcataataa ctgctcccaa  780
tatcgggatt agaacgattt tcagctcaaa atatggaaaa ttggttacat aaaccgcata  840
tttgtagcat taatcttgaa cagctatatg gcattaaaaa aaaatatata tatacattgt  900
tttttctctc gaagtttctc tttttgtttc taaaatccgg aatataattt aaaaaaccac  960
ataaatttca atttgcagta cgagttcccc ccgaatcaca atg ccg gca aca ccg  1015
                                            Met Pro Ala Thr Pro
                                            1               5
```

```
gtg cgt gct tca agt act cga ata agc aga cgt aca tca tca aga tca   1063
Val Arg Ala Ser Ser Thr Arg Ile Ser Arg Arg Thr Ser Ser Arg Ser
            10              15                  20
```

```
gtg gct gat gat cag cca tca act tcg tct gcg gtg gct cca cct cct   1111
Val Ala Asp Asp Gln Pro Ser Thr Ser Ser Ala Val Ala Pro Pro Pro
            25              30                  35
```

```
tca ccc att gcc ata gaa act gat gaa gat gcg gta gtt gag gag gag   1159
Ser Pro Ile Ala Ile Glu Thr Asp Glu Asp Ala Val Val Glu Glu Glu
        40              45              50
```

```
aaa aag aag aaa aag aca tca gat gat ttg gaa att atc act cca aga   1207
Lys Lys Lys Lys Lys Thr Ser Asp Asp Leu Glu Ile Ile Thr Pro Arg
    55              60              65
```

```
act cca gtc gat cgg cga att ccc tac att tgc tcg att ctt ttg act   1255
Thr Pro Val Asp Arg Arg Ile Pro Tyr Ile Cys Ser Ile Leu Leu Thr
70              75              80                  85
```

```
gaa aat cga tcg att cgc gat aaa tt gtacgatttt ttaaatttaa          1301
Glu Asn Arg Ser Ile Arg Asp Lys Leu
                90
```

```
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tctgaaaaaa atctgctatt ttcagtggaa aggcaaaata ccgcgaagcg cagcaagcgc  1841
gctctaataa ttattccgct tcgagaagag cgtgtattat ttcattgtta catttcaaaa  1901
```

Fig. 19A

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```
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                          Val Leu Ser Ser Gly Pro Val Arg Gln Glu
                           95                  100


gat cac gaa gaa cag att gct cga gct caa cgg ata cag cca gtt gtc   2001
Asp His Glu Glu Gln Ile Ala Arg Ala Gln Arg Ile Gln Pro Val Val
105                 110             115                 120


gat caa att caa cga gtc gag caa at gtatgtgaag ctgaaaaatt          2047
Asp Gln Ile Gln Arg Val Glu Gln Ile
                125


gcaccacaaa tcaattattc taatcttgtt ttacag c ata ctc aat ggt tca gtg 2102
                                           Ile Leu Asn Gly Ser Val
                                           130                 135


gaa gat att ctg aaa gat cct cga ttc gca gta atg gca gat ctc aca   2150
Glu Asp Ile Leu Lys Asp Pro Arg Phe Ala Val Met Ala Asp Leu Thr
              140             145                 150


aaa gaa cca cca cca aca cct gca cct cct cct cca atc cag aag aca   2198
Lys Glu Pro Pro Pro Thr Pro Ala Pro Pro Pro Pro Ile Gln Lys Thr
              155             160                 165


atg caa ccg att gag gtg aaa att gag gat tca gag ggc tca aat acg   2246
Met Gln Pro Ile Glu Val Lys Ile Glu Asp Ser Glu Gly Ser Asn Thr
          170             175             180


gct caa ccg agt gtt ctg ccc agt tgt gga gga gga gag acg aat gtg   2294
Ala Gln Pro Ser Val Leu Pro Ser Cys Gly Gly Gly Glu Thr Asn Val
      185             190             195


gaa aga gcc gcc aaa aga gtgagttttg aagatagatt ggtgtgtaaa          2342
Glu Arg Ala Ala Lys Arg
200                 205


aaatgaatgt ttatatattc actgcaactt tttcctcacg agggacgagg aaaagtggtt 2402
tctaggccat ggccgaggtg ccgacaagtt tcagcggcca tttatcttgc tttgttttcc 2462
gcctgttttc tttcgttttt catcgatttt tttcgttttt tcttaataaa actgataaat 2522
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ccgtaatcca tcatattgca ttgaccactt tcaccgctgc ttgcccactg aatacatgat 2942
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aatttcaacg ctcgctaata ttcctaattt gaaccgcgct tttgtccgcg ccgcactctg 3422
tagaattgca tccgcgctgt ttccttcctc ttccggcgcc ctacttcttt tcgattggaa 3482
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Fig. 19B

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```
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tgctttttta ggcccaaatt ggtccaaaac taccgaattt tgtaatgaga cgttctgaaa 3842
atttatccaa aaaatgttat ggcggttcaa agttcggcaa aatagggccc attttcagct 3902
aaaatcaaat ttttttttcc aacttttttcg gtgtcgcaac gtctggagcc taatttttat 3962
ttattaatca ctttttaata aatattgtag cctttgatta ggcgtttatt cgctgattta 4022
agtacattta tggtttttgg ggcacaaata aaagtttcat tttatgcccc aaaaaccata 4082
aatgtactta aatcagcgaa taaacgccta atcaaaggct acaatattta ttaaagagtg 4142
atgaataaat aaaaattagg ttccagacgt tgcgacaccg aaaaagttgg aaaaaatttt 4202
gatttagct gaaaatgtgc cttattttgc cgcgaacttt gaaccgccat aacttttttt 4262
gagaaagaaa ttttcagaac gtctcattac gaaattcggt agtttttaaac caatttgggt 4322
ctaaaaagtt tcaaattcca ataaaacata ccaaagtctt gtgaaattac aataaactat 4382
tcctaaacgt attataatcc attctcaatt cttgcag gaa gcg cat gta ttg gct 4437
                                           Glu Ala His Val Leu Ala
                                                             210
```

```
cga atc gcc gag ctc cgt aag aac ggc tta tgg tcg aac agt cgt ctg   4485
Arg Ile Ala Glu Leu Arg Lys Asn Gly Leu Trp Ser Asn Ser Arg Leu
            215                 220                 225
```

```
cca aag tgc gtc gaa cct gaa cgt aat aaa acg cat tgg gat tat cta   4533
Pro Lys Cys Val Glu Pro Glu Arg Asn Lys Thr His Trp Asp Tyr Leu
            230                 235                 240
ctg gaa gag gtc aaa tgg atg gca gtt gat ttc cga acc gag acg aat   4581
Leu Glu Glu Val Lys Trp Met Ala Val Asp Phe Arg Thr Glu Thr Asn
            245                 250                 255
```

```
acg aag cga aaa atc gcc aaa gtt ata gct cac gcc att gcg aaa cag   4629
Thr Lys Arg Lys Ile Ala Lys Val Ile Ala His Ala Ile Ala Lys Gln
260                 265                 270                 275
```

```
cac cgc gac aag cag atc gag att gag aga gcc gcc gaa cgg gag atc   4677
His Arg Asp Lys Gln Ile Glu Ile Glu Arg Ala Ala Glu Arg Glu Ile
                280                 285                 290
```

```
aag gag aag cga aaa atg tgt gca gga atc gcg aag atg gta cgg gat   4725
Lys Glu Lys Arg Lys Met Cys Ala Gly Ile Ala Lys Met Val Arg Asp
                295                 300                 305
```

```
ttc tgg tcg tct acg gat aaa gtt gtg gat att cga gcg aag gaa gtt   4773
Phe Trp Ser Ser Thr Asp Lys Val Val Asp Ile Arg Ala Lys Glu Val
                310                 315                 320
```

```
ctg gag tcg agg ctc agg aag gcg aga aat aag cat ttg atg ttt gta   4821
Leu Glu Ser Arg Leu Arg Lys Ala Arg Asn Lys His Leu Met Phe Val
                325                 330                 335
```

```
att gga caa gtc gat gaa atg agc aat att gtg caa gaa gga ctt gtt   4869
Ile Gly Gln Val Asp Glu Met Ser Asn Ile Val Gln Glu Gly Leu Val
340                 345                 350                 355
```

```
tca tcg tcg aaa tcc cca tca att gca tcg gat cga gat gat aaa gat   4917
Ser Ser Ser Lys Ser Pro Ser Ile Ala Ser Asp Arg Asp Asp Lys Asp
                360                 365                 370
```

Fig. 19C

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```
gaa gaa ttc aaa gca cct ggc tct gat tca gaa tct gac gat gag cag   4965
Glu Glu Phe Lys Ala Pro Gly Ser Asp Ser Glu Ser Asp Asp Glu Gln
        375                 380                 385

aca att gca aac gcg gaa aag tca cag aaa aag gaa gat gtt cga cag   5013
Thr Ile Ala Asn Ala Glu Lys Ser Gln Lys Lys Glu Asp Val Arg Gln
        390                 395                 400

gaa gtt gat gct ctt caa aac gag gca act gtg gat atg gat gac ttt   5061
Glu Val Asp Ala Leu Gln Asn Glu Ala Thr Val Asp Met Asp Asp Phe
    405                 410                 415

ttg tac act tta ccg ccg gaa tat ctg aag gct tat ggt ctg acg cag   5109
Leu Tyr Thr Leu Pro Pro Glu Tyr Leu Lys Ala Tyr Gly Leu Thr Gln
420                 425                 430                 435

gag gat ttg gag gag atg aag cgc gag aaa ttg gag gag cag aag gct   5157
Glu Asp Leu Glu Glu Met Lys Arg Glu Lys Leu Glu Glu Gln Lys Ala
                440                 445                 450

cgg aag gaa gct tgt ggt gat aat gag gag aaa atg gag att gat gaa   5205
Arg Lys Glu Ala Cys Gly Asp Asn Glu Glu Lys Met Glu Ile Asp Glu
        455                 460                 465

gttcgtagga tgctcctaaa aaaattacct aaaaaaaatc gattttccct ggaaaaaatc 5265
ctctggaaat gacccgaaac gtcatggcgg ctcgaaattt tgaaaaaaaa aacccccaa  5325
atttccagct aaaatctcaa attttattgc atattttggt agttcttttg ttgtccgagg 5385
tgcgtttttc agctgaaaat gtacctgaat ctgcaagtaa acgaccaata tatgcaataa 5445
atgatgataa ttaatttccg atactgaaat gtgggcgaaa tttgagattt cgactgaaaa 5505
cgtcttaaaa atcacccaaa acccggcttt accgcacgaa ggtttgaaga aaatggccaa 5565
tttttagcca aaatctcaaa tttcgtccac ttttcagtca gaaattagtt ttttgaaatt 5625
aattaacacc ttttattgca tattttcgtc gtttattcgt tgatcgaggt gctttttcgg 5685
tcgatgggtg cacaaattcg gtaattgtgc atccatcggc tgaaaatgct ccagaatttg 5745
cgaatgaacg gtgaaaattt aagattttag attgaaataa gccgtttttt agagaaaatt 5805
ggtcgttttg agacattaaa ttcaatttaa atcccctctt tattttcag agc cca tca 5863
                                                       Ser Pro Ser
                                                               470

tca gat gct caa aag cct tcc acc tca agc tca gat ctc acc gcc gag   5911
Ser Asp Ala Gln Lys Pro Ser Thr Ser Ser Ser Asp Leu Thr Ala Glu
            475                 480                 485

cag ctt caa gat cca aca gct gaa gac ggc aac ggt gat ggt cat ggt   5959
Gln Leu Gln Asp Pro Thr Ala Glu Asp Gly Asn Gly Asp Gly His Gly
            490                 495                 500

gta ctt gaa aac gtg gat tac gtg aag ctc aac agt cag gat agt gat   6007
Val Leu Glu Asn Val Asp Tyr Val Lys Leu Asn Ser Gln Asp Ser Asp
        505                 510                 515

gaa cga caa caa gag ttg gcg aat atc gca gaa gaa gcg ctg aaa ttc   6055
Glu Arg Gln Gln Glu Leu Ala Asn Ile Ala Glu Glu Ala Leu Lys Phe
    520                 525                 530
```

Fig. 19D

Title: RB PATHWAY AND CHROMATIN REMODELING
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```
cag cca aaa gga tat aca ctt gag acg aca caa gtc aag acg ccc gta    6103
Gln Pro Lys Gly Tyr Thr Leu Glu Thr Thr Gln Val Lys Thr Pro Val
535             540             545             550

cca ttc ctg att cga gga caa ctg aga gaa tat caa atg gtt gga ttg    6151
Pro Phe Leu Ile Arg Gly Gln Leu Arg Glu Tyr Gln Met Val Gly Leu
            555             560             565

gat tgg atg gtt aca ctt tat gag aag aat ttg aat gga att ctt gcc    6199
Asp Trp Met Val Thr Leu Tyr Glu Lys Asn Leu Asn Gly Ile Leu Ala
            570             575             580

gac gag atg ggc ctg gga aag acg att caa acg att tcc ctg ctg gct    6247
Asp Glu Met Gly Leu Gly Lys Thr Ile Gln Thr Ile Ser Leu Leu Ala
            585             590             595

cat atg gct tgt agt gaa tcg att tgg gga cca cac ttg att gtt gtg    6295
His Met Ala Cys Ser Glu Ser Ile Trp Gly Pro His Leu Ile Val Val
            600             605             610

ccg acg tct gtc att ctg aat tgg gag atg gag ttc aag aaa tgg tgt    6343
Pro Thr Ser Val Ile Leu Asn Trp Glu Met Glu Phe Lys Lys Trp Cys
615             620             625             630

ccg gct ctg aag att ttg acg tat ttt ggt acg gcg aag gag cgt gcc    6391
Pro Ala Leu Lys Ile Leu Thr Tyr Phe Gly Thr Ala Lys Glu Arg Ala
            635             640             645

gag aag cgg aag gga tgg atg aag ccg aat tgt ttc cat gtg tgc atc    6439
Glu Lys Arg Lys Gly Trp Met Lys Pro Asn Cys Phe His Val Cys Ile
            650             655             660

aca tca tac aag acg gtt act caa gat att aga gct ttt aag cag agg    6487
Thr Ser Tyr Lys Thr Val Thr Gln Asp Ile Arg Ala Phe Lys Gln Arg
            665             670             675

gtgcgtagaa attttgaaga tttgcggcga atttggcgaa tttgcataat ttttttaaaa 6547
ccaattttac cgataattgc gaaattttc aatttatac agtggtcgga aattgctata 6607
attagtataa ttttttgcaaa aattggtact ttttttcgaaa ttttgaacca ccataaaaca 6667
ttttttgaaca attttttaaga ggtttaataa cgaaattcgt tcatttgaac acattttggc 6727
gatatgaatc gcccgaaaat gtccccaat agacctaatt tcttaacaaa aatttaaaaa 6787
aaaatggccc aaaattgtct caaaatttcg aaaaaaaaac cgtaatttca gctgaaatct 6847
caaaatttgc caaattttcc gtctcacgga gatcagaaaa agtttttttgc attttttttgt 6907
ggtttatttt agcgttatttt cgttaattta gatacatttt agcccaattt ttgcaaaat 6967
tatactaatt atagcaattt ctgacccctg acaaactttg aaattatcgg taaacttggt 7027
ataaatggtt ttttttccaaa tttttaaagc gatattaaag gtggagtacc acaatttgag 7087
gctttgtttt tttttttggaa cccaaattgg tccaaaacta ccgaatttcg taatgagacg 7147
ctctgaaaat ttctttctca aaaaaaaagt tacggcggtt caaagttcgc ggcaaaataa 7207
ggcccatttt cagctaaaat caaaatttttt tcccaacttc tcggtgtctc aacgcctgga 7267
```

Fig. 19E

Title: RB PATHWAY AND CHROMATIN REMODELING
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```
acctaatttt tatttattca tcactttta ataaatattg tggtctttga ttgggctttt 7327
attcgttgat ttaagtacat ttatggtcag tggggcacaa aatgtaactt ttttcccaa 7387
agaccataaa tgtactttaa tcaacgaata aacgcccaat caaagaccac aatatttatt 7447
taaaagtaat gaataaataa taattaggtt ccagacgttg cgacaccgag aagttggaaa 7507
attttttat tttagctgaa taagggcctt attgtctcaa actttgaacc gccataactt 7567
tttttgaga acgtctcgtt acgaaattcg gtagttttgg accaatttgg gtctaaaaaa 7627
acaaagtctc aaatttcttg ttagagattt tttaaaaatt gatattttt ttttcag gcc 7687
                                                               Ala
```

```
tgg cag tac cta att ctc gat gaa gct caa aat atc aaa aac tgg aag   7735
Trp Gln Tyr Leu Ile Leu Asp Glu Ala Gln Asn Ile Lys Asn Trp Lys
680             685         690                     695

tcc caa cgt tgg cag gct ctt ctg aat gtc cgt gct cga cgt cgc ctt   7783
Ser Gln Arg Trp Gln Ala Leu Leu Asn Val Arg Ala Arg Arg Arg Leu
                700             705             710

ctc ctg acc gga act cca ctt cag aac tct cta atg gaa ctg tgg tcg   7831
Leu Leu Thr Gly Thr Pro Leu Gln Asn Ser Leu Met Glu Leu Trp Ser
                715             720             725

ttg atg cat ttt ttg atg cca aca ata ttc tca agt cat gat gat ttc   7879
Leu Met His Phe Leu Met Pro Thr Ile Phe Ser Ser His Asp Asp Phe
        730             735             740

aag gat tgg ttc tcg aat ccg ttg aca ggg atg atg gaa gga aat atg   7927
Lys Asp Trp Phe Ser Asn Pro Leu Thr Gly Met Met Glu Gly Asn Met
        745             750             755

gaa ttc aat gct cca cta atc gga cga ctt cac aaa gtg ctc cgt ccg   7975
Glu Phe Asn Ala Pro Leu Ile Gly Arg Leu His Lys Val Leu Arg Pro
760             765             770             775

ttt att ctg cgg cgg ctc aag aag gaa gtt gag aag cag ctg cca gag   8023
Phe Ile Leu Arg Arg Leu Lys Lys Glu Val Glu Lys Gln Leu Pro Glu
                780             785             790

aag act gag cat att gtg aat tgt tcg ttg tca aag cgg cag aga tac   8071
Lys Thr Glu His Ile Val Asn Cys Ser Leu Ser Lys Arg Gln Arg Tyr
                795             800             805

ctg tac gat gac ttt atg agt cgt aga tca aca aag gag aat cta aag   8119
Leu Tyr Asp Asp Phe Met Ser Arg Arg Ser Thr Lys Glu Asn Leu Lys
        810             815             820

tct gga aat atg atg tcg gtg ctc aac att gtg atg caa ctc cga aaa   8167
Ser Gly Asn Met Met Ser Val Leu Asn Ile Val Met Gln Leu Arg Lys
        825             830             835

tgt tgt aat cat ccg aat ctc ttc gag ccg cgg cca gtt gtt gct ccg   8215
Cys Cys Asn His Pro Asn Leu Phe Glu Pro Arg Pro Val Val Ala Pro
840             845             850             855
```

Fig. 19F

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```
ttc gtc gtt gag aag ctt cag ctc gat gtt ccg gct cgt ctc ttt gaa    8263
Phe Val Val Glu Lys Leu Gln Leu Asp Val Pro Ala Arg Leu Phe Glu
            860                 865                 870


att tcg cag caa gat ccc tcc tcc tcc tca gct agt caa att ccg gaa    8311
Ile Ser Gln Gln Asp Pro Ser Ser Ser Ser Ala Ser Gln Ile Pro Glu
            875                 880                 885


att ttc aat tta tcc aaa atc ggc tat caa tct tcc gtt cga tct gca    8359
Ile Phe Asn Leu Ser Lys Ile Gly Tyr Gln Ser Ser Val Arg Ser Ala
            890                 895                 900


aaa cca ctc atc gaa gag ctt gaa gca atg agc act tat ccg gag cca    8407
Lys Pro Leu Ile Glu Glu Leu Glu Ala Met Ser Thr Tyr Pro Glu Pro
        905                 910                 915


cga gca cca gaa gtt ggc gga ttt cgg ttc aat cgg acg gct ttt gtt    8455
Arg Ala Pro Glu Val Gly Gly Phe Arg Phe Asn Arg Thr Ala Phe Val
920                 925                 930                 935


gca aag aat ccg cat acg gaa gag tcg gag gac gaa ggt gtt atg aga    8503
Ala Lys Asn Pro His Thr Glu Glu Ser Glu Asp Glu Gly Val Met Arg
            940                 945                 950


agt cgt gtt ctg gtgaatttttt aggaaaattg agaaaatgat ctaattgttg       8555
Ser Arg Val Leu
            955


aattttttaa agaatttatg ggccacaagc cgatttgccg gaaattttga tttttggcga 8615
tttgccgaaa attttgattt ttggcgattt gccagaaatt ttgattttttg gcaattatcc 8675
gatttgccgg aaattttgat ttttggcgat ttgccagaaa tttttgatttt tggcaattat 8735
ccgatttgcc ggaaattttg aattttggca atttttccgat ttgccggaaa tttttgatttt 8795
tggcaatttg ccgaattgcc ggaaattttg attttggca atttgccgaa ttgccggaaa 8855
ttttgattttt tggggatttg ccggaaattt tgattttttgg caatttgcct atttgtcgga 8915
aattttgatt tttggcaatt gccgatttg tcggaaattt tgattttttgg caatttgccg 8975
atttgccgga aattttgatt tttggcaatt ttccgatttg ccaaaaattt tgattttttgg 9035
cgatttgccg atttgccgga aaaacatttt gtgagccaat tttctcgaaa tttgggcttc 9095
aatattttca aattattcca aattttccac tgattccgaa tatctaagta aaaaaaaatt 9155
ccctgatttt atatttcagc ttaaaatcgc taattttcgc gtcagagacg acgtcatgtg 9215
tcgatttact ggatttttaa tctttgtcgg atgctaattt ccgttttttca acgagtttcc 9275
ttcatttcca tcggtttttg acgaagtttt ctttgaaaat atgttcttaa ggtcaattaa 9335
acgtttatt atcaaaaaaa actagcaaaa ttggctttaa aaacacattt tcacagaaaa 9395
ctccgacaaa aaccgacgaa aatgaaggaa accccccgtt tgaaaacaga aattagcatc 9455
tgataaagat taaaatcccg taaatcgaca catggcgtct ggcgtctctg cacgaaaag 9515
tcgcgatttt aagctgacat acaaaaaaag agggatatat ttttttacga atttttcaca 9575
tagatattcg aaatcagggg ggaaaatttg gagaaatttg agaaaatttc tcagatttcg 9635
gattaaaaat attcaatttt tgtttttctta tattaaaaaa aaattaactt ttataatttt 9695
tcag cca aaa cca att aat gga aca gct caa cca ctt caa aat gga aat    9744
    Pro Lys Pro Ile Asn Gly Thr Ala Gln Pro Leu Gln Asn Gly Asn
             960                 965                 970


tca ata cca caa aat gct cca aat cgt cca caa act tca tgc att cgt    9792
Ser Ile Pro Gln Asn Ala Pro Asn Arg Pro Gln Thr Ser Cys Ile Arg
            975                 980                 985
```

Fig. 19G

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```
tca aaa acc gtc gta aat aca gtt cca ctg acc atc tcc acc gat cga    9840
Ser Lys Thr Val Val Asn Thr Val Pro Leu Thr Ile Ser Thr Asp Arg
        990               995               1000

agt ggt ttt cat ttt aat atg gcc aat gtt gga aga ggt gtt gtt cgt    9888
Ser Gly Phe His Phe Asn Met Ala Asn Val Gly Arg Gly Val Val Arg
        1005              1010              1015

ttg gat gat tca gca cgt atg agc cca ccg ctc aaa cgt cag aag ctc    9936
Leu Asp Asp Ser Ala Arg Met Ser Pro Pro Leu Lys Arg Gln Lys Leu
    1020              1025              1030

acc gga act gca acg aat tgg agt gat tat gtt ccg cga cac gtt gtt    9984
Thr Gly Thr Ala Thr Asn Trp Ser Asp Tyr Val Pro Arg His Val Val
1035              1040              1045              1050

gaa aag atg gaa gaa tcg aga aaa aac cag ctg gaa att gtt cga agg    10032
Glu Lys Met Glu Glu Ser Arg Lys Asn Gln Leu Glu Ile Val Arg Arg
              1055              1060              1065

cga ttt gag atg att cgt gct ccg att att cca ctg gaa atg gtt gcg    10080
Arg Phe Glu Met Ile Arg Ala Pro Ile Ile Pro Leu Glu Met Val Ala
              1070              1075              1080

ctg gtt cga gag gaa att att gca gaa ttt cca cgt ttg gct gtg gaa    10128
Leu Val Arg Glu Glu Ile Ile Ala Glu Phe Pro Arg Leu Ala Val Glu
        1085              1090              1095

gag gac gag gtt gtg cag gag agg ctt ttg gag tat tgc gag ttg ttg    10176
Glu Asp Glu Val Val Gln Glu Arg Leu Leu Glu Tyr Cys Glu Leu Leu
    1100              1105              1110

gtg caa aggtagaatt ttgaaaatta ttactttgct tttttttaaa ccaaaattgg    10232
Val Gln
1115

cccaaaacta ccgaatttcg taatgagaca ttctgaaagc ttctcaaaaa aaaagttttg 10292
gccgctcaaa gttcgggaaa ataaggccca ttttcagctg aaatcaaaat tttttccaac 10352
ttctcggtgt cgcaacgtct ggaactaaaa ttttggaaaa cgagaaattt tccatttttt 10412
gcaagctgaa aaatcaaagt ttttttttcc tcaaaattgg acaaacaaaa aaattttttt 10472
ttgaaaattg atcgaaaaaa ttcaaaattt ctataatttt tcgatttttt aaataaaact 10532
ttcatcattt ttcttccaaa tttagttttc tcgattttaa ctttttttcaa aaaaaaattt 10592
tttaatacga aaaaaattca attttagctc taattctttt ttagacccaa attggtccaa 10652
aactaccgaa tttcgtaatg agacgttctg aacatttctc aaaaaaaagt tatgacggtt 10712
caaagttcgg caaaataagg cccatttttca tataaaatca aattttttttt ctaacttctc 10772
ggtgtcacaa cgtctggaac ttaattttta tttaattatt acttttcaat aaatattgtg 10832
gtcttttatt aggcgtttat ttgttgattt aagtacattt atggtcaagt ggggcccaaa 10892
taaaagttac atttgtgcc cacatgacca taaatgtact taaatcaacg aataaacgcc 10952
taatcaaagg ccacaatatt tattaaaaag tgttgaataa ataaaaatta ggttccagac 11012
attgtgacac cgagaagtta aaaaaaattt tgattttagc tgaaaatggg ccttatttttg 11072
ctgaacttta aaccgctata actttttttt gagaaatttt cagaacgtct cattacgaaa 11132
ttcggtagtt ttggaccaat ttgggtctaa aaaagaatta gagctaaaat tgaatttct 11192
tcgtattaaa aatttttttt ttgaaaaaag taaaaatcga gaaaactaaa tttggaagaa 11252
aaatgatgaa aatttttattt aaaaaaatcga aaaattatag aaattttgat cgatttttc 11312
gatcaatttt caataaaaaa ttttttgttt gtccaatttt gaggaaaaaa aaaactttga 11372
```


Fig. 19H

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```
tttttcagct tacaaaaaat ggaaagtttc tcgttttcca atttttttgat gtggattttt  11432
atgagaaaaa atatataatg tcacaaaaaa tagattatta tctaaaaatc gaaaaaatta  11492
aattttccag ttttcaggaa aaaaatcgtt aagaaattgt ttttccatta aaggtggagt  11552
accgaatttt gagacgctgc tttttttagac ccaaaatggt ccaaaactac cgaatttcgt  11612
aatgatacgc tctgaaaaat tttcaaaaaa aaagttgtga ccgctcaaag ttttggaaaa  11672
atggcatatt tttagctaaa atctcaaatt ttggcaactt atcggtgtcg cagcggttgg  11732
aacttaattt ttatttaatt gtcattcatt aatgcatgtt ttggcatttc attatgtgtt  11792
atttcgttga ttgagatgct ttttgtgcct gcatcgacca aaaaaccatc tcaatcaacg  11852
aaataacaca taataaaatg ccaaaatatg cattaaagga tgataatcaa ataaaaatta  11912
agtttcaacc gctgcgacac cgctaagttg ccaaaatttg agattttagc taaaaatggt  11972
ccattttttct aaaacttttga gcggtcacaa cttttttttt gagaaattt cagagcgtct  12032
cattacgaaa attggtaggt tcggaccaat ttgggtctaa aaaagcagcg tctcaaaatt  12092
cggtacttca cctttaaagt tttcaattta aagtataaat tatccaatca aaaattgacg  12152
aaaaaatttt ttaaaaattt tttcttccga aaaaaaaatt aattttaatt tttgtt aga  12211
                                                                    Arg
```

```
ttc gga atg tac gtc gaa cca gtg ctg acc gat gct tgg cag tgt cgt   12259
Phe Gly Met Tyr Val Glu Pro Val Leu Thr Asp Ala Trp Gln Cys Arg
        1120             1125             1130
```

```
cca tca tcg tct ggt ctt cca tca tat att cgc aac aat tta tca aat   12307
Pro Ser Ser Ser Gly Leu Pro Ser Tyr Ile Arg Asn Asn Leu Ser Asn
        1135             1140             1145
```

```
atc gag ctg aat tct cgt tct ctt ctc ctc aac acc tcc act aat ttc   12355
Ile Glu Leu Asn Ser Arg Ser Leu Leu Leu Asn Thr Ser Thr Asn Phe
1150             1155             1160             1165
```

```
gat acc cga atg tcg atc tca cgt gct ctt caa ttc cca gaa ctc cgt   12403
Asp Thr Arg Met Ser Ile Ser Arg Ala Leu Gln Phe Pro Glu Leu Arg
            1170             1175             1180
```

```
ctg atc gag tac gat tgt gga aag ctt cag acg ttg gct gtt ctg ctt   12451
Leu Ile Glu Tyr Asp Cys Gly Lys Leu Gln Thr Leu Ala Val Leu Leu
            1185             1190             1195
```

```
cgt cag ttg tac ctg tac aag cac aga tgt ctg atc ttc acg caa atg   12499
Arg Gln Leu Tyr Leu Tyr Lys His Arg Cys Leu Ile Phe Thr Gln Met
        1200             1205             1210
```

```
tca aag atg ctc gac gtt ctg cag acc ttc ctt tct cat cac ggt tat   12547
Ser Lys Met Leu Asp Val Leu Gln Thr Phe Leu Ser His His Gly Tyr
        1215             1220             1225
```

```
cag tat ttc cgc ctc gac ggt acc act ggt gtc gaa caa aga cag gcg   12595
Gln Tyr Phe Arg Leu Asp Gly Thr Thr Gly Val Glu Gln Arg Gln Ala
1230             1235             1240             1245
```

```
atg atg gag cgg ttc aac gcg gat ccc aag gtg ttt tgc ttc att ctg   12643
Met Met Glu Arg Phe Asn Ala Asp Pro Lys Val Phe Cys Phe Ile Leu
            1250             1255             1260
```

```
tcg acg aga tcc ggt ggt gtt gga gtc aat cta acc ggt gct gac act   12691
Ser Thr Arg Ser Gly Gly Val Gly Val Asn Leu Thr Gly Ala Asp Thr
            1265             1270             1275
```

Fig. 19I

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```
gtg atc ttc tac gat tcg gat tgg aat ccg acg atg gat gct cag gct   12739
Val Ile Phe Tyr Asp Ser Asp Trp Asn Pro Thr Met Asp Ala Gln Ala
        1280             1285             1290

cag gat aga tgt cat cgt atc gga cag acg agg aat gtc tcg att tat   12787
Gln Asp Arg Cys His Arg Ile Gly Gln Thr Arg Asn Val Ser Ile Tyr
    1295             1300             1305

cga ttg att tcc gag cga aca att gag gag aat att ctg aga aag gca   12835
Arg Leu Ile Ser Glu Arg Thr Ile Glu Glu Asn Ile Leu Arg Lys Ala
1310             1315             1320             1325

aca cag aag cgg cga ctt gga gag ttg gca att gac gag gct ggc ttc   12883
Thr Gln Lys Arg Arg Leu Gly Glu Leu Ala Ile Asp Glu Ala Gly Phe
            1330             1335             1340

aca ccc gag ttc ttc aaa caa tct gac agt att cgg gat ctt ttt gat   12931
Thr Pro Glu Phe Phe Lys Gln Ser Asp Ser Ile Arg Asp Leu Phe Asp
            1345             1350             1355

gga gag aat gtg gaa gtg act gct gtg gca gat gtt gcg acg acg atg   12979
Gly Glu Asn Val Glu Val Thr Ala Val Ala Asp Val Ala Thr Thr Met
            1360             1365             1370

agc gag aaa gaa atg gag gtt gcg atg gca aag tgt gaa gat gaa gct   13027
Ser Glu Lys Glu Met Glu Val Ala Met Ala Lys Cys Glu Asp Glu Ala
        1375             1380             1385

gat gtg aat gcg gcg aag att gcg gtg gcc gag gcg aac gtt gat aat   13075
Asp Val Asn Ala Ala Lys Ile Ala Val Ala Glu Ala Asn Val Asp Asn
1390             1395             1400             1405

gcg gag ttt gat gag aaa tca ttg ccg ccg atg agc aat ttg caa gga   13123
Ala Glu Phe Asp Glu Lys Ser Leu Pro Pro Met Ser Asn Leu Gln Gly
            1410             1415             1420

gat gag gag gct gat gag aag tat atg gag ttg ata caa c aggtaaaatt  13173
Asp Glu Glu Ala Asp Glu Lys Tyr Met Glu Leu Ile Gln
            1425             1430

cggcggaaat cggaaatttt cccatttaga atatcaaatt ttgcccgatt gtgtcgtttt 13233
ttgatttttc gatttattcg atttgttttt gagggaaaat cggaaaaatg ttcagaaaat 13293
taaccataac atgtgatctt tttaaaatct tagcgcaaat gtcttctaaa aaataaagaa 13353
tgaccaaaaa ttttaagcta atttttgaaa aaccaaagaa aaaatttaga tttttcgatg 13413
ttttccgaga caaaaagaca aaaacggaaa ttgtcgaaaa tgaatgaaat ttttaatttt 13473
tcagcaaaaa aaaaatagta cttaatttta aaaatgtga tcatttcggt aggaaaatct 13533
ggaaaaatcg attttcaaac aaaaaaaaac cgagcctcta caatcttttt ttttcccgaa 13593
atctccagaa cttctcacaa taacaactat ataaatttca aaatttc ag ctc aaa    13648
                                                       Leu Lys
                                                       1435

cca atc gaa cga tat gcc att aac ttt ctt gag aca cag tac aag cca   13696
Pro Ile Glu Arg Tyr Ala Ile Asn Phe Leu Glu Thr Gln Tyr Lys Pro
        1440             1445             1450
```

Fig. 19J

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```
gaa ttt gag gaa gaa tgc aaa gag gca g aggtatatta ttccattcat       13744
Glu Phe Glu Glu Glu Cys Lys Glu Ala
    1455                1460


ctgacttttt ttttttttt ttaaatttaa atttcaccaa attaattac ag gct ctt  13801
                                                      Glu Ala Leu
                                                              1465


atc gac caa aaa cgc gaa gaa tgg gac aaa aat ctc aac gat acc gcc  13849
Ile Asp Gln Lys Arg Glu Glu Trp Asp Lys Asn Leu Asn Asp Thr Ala
            1470            1475            1480


gtc att gac ctc gac gat tcg gat agt ctg ctg ctc aac gat cct tcg  13897
Val Ile Asp Leu Asp Asp Ser Asp Ser Leu Leu Leu Asn Asp Pro Ser
        1485            1490            1495


act tct gcc gat ttt tat cag agc tca agt ctt tta gac g aggtacgcga 13947
Thr Ser Ala Asp Phe Tyr Gln Ser Ser Ser Leu Leu Asp
        1500            1505            1510


tcgtcgtcgt cgcagcagca gccttctcca aaaagccgct caaaaaccgg caaaaaagcc 14007
tcaaaacttc caaattcgtg ctcgctcccc gtctaagcgt aaatctcagg ctccttcctt 14067
cgatccatat gtttcgtacg caccgcacgc gctcgcttct cccccggatt ccccgcgtaa 14127
gagaagatca cgtggtgcgc gtagtttagg tagtggtggt ggtggtggtg gtggtagtag 14187
atctgttgga agacctgccc gccgatcagt gaagaaagaa gaatcagatg atgatgatga 14247
ggattattgc caagaagagg aagtgaagcg aaatccggca gaaaaggtcc cgccgaaaag 14307
aaaacgagtt gtgtttgtgg aacctccaga ggtgaagccg ccggagccga aaaaacgagt 14367
tgttgttcct gctccatcat catcatcatc agctctaact actcttccac aacaaggacc 14427
gctgatttcg ttgccaaaag ctgtgccagt tgtacctcgg ccccaacaac aagcaccacc 14487
acagctcatc aaaaagcacc agcagactct gatgcctgtg aaggtgctca agattagtgg 14547
tggtggtggt ggtactccag gaccatccag tgtatcgcca ggtccatcaa tcctccgaag 14607
aaccgttgtt ccaggcatag gcgctggtgg tgttggacgc ctaccgcttg tcagaatgcc 14667
tgttcgccct ccatttcctg gctcgcaagc tcctgctcca ccgctgagaa gtggtgttgc 14727
tccaacagct cctgcagcag ctccacgcca gttcgtcgtt ccgtcgtcga gagttcgagt 14787
tatcacgacg agaactccgg tcgccaccac catggtgcaa caacaacaaa gcccgagccc 14847
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acctccagat cgcccaggat ttggaatcta tgagaagccg agattctcac ttggatcacg 14967
aagaagccgt ggagattcgg gcccggaaga tccggcgcca ccacagccac caccacccac 15027
cacttctagg ccaccgccac aagcctaggc gctaggattt tccttttttt tttgttgatt 15087
tttgctcttt ttttgctctc tcatgatttt ataatctcat tttgctttaa tatttccatt 15147
tttttggatg tgtggaattt ttttttttga aaatcgggaa aaaacgaaaa atttgaactt 15207
tttggtgatt ttcagagaaa aatccgtttt taaatgaaaa aatcggaata attcagattt 15267
ttcgaaaaaa aaaaccgaga aaatttcaaa ttttcagttt ttttttttcaa aaaatcgaaa 15327
aaaaaagtaa attttcagaa ttatcagcca agttttttgcg attttttttgaa aaatttcaat 15387
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tttcgaaaaa aaaaacgaag aaagtttcaa atttttagct ttttttcaaaa aatcgaaaat 15507
cggaatttttt ttaatttttc gaataaaaaa aatcgaagaa attccaaaac tttgcgtttt 15567
ttcttgaaat tatctgaaaa ccggaatttt ttttcaaaat tcgccatttt ttgcgaattt 15627
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tttcttttgt tccaaaaagt caaaaaccga acaattattt atttcaaaaa ctctaaaaat 15747
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cggttatttt tcacacacac acattttcct cccgagcggt tctttttttc atgagttctc 15987
ccatgttttg tttttatatt tgagacattt ttttttgttg ataagtttca acttcttctt 16047
```

Fig. 19K

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```
cttcttctga ctataaacgt ttttctccat gttttttgcc tgttttctgc cgattttttg 16107
acacccaaaa ttttttttca ttttcgctcg aaaatgcacg tcgttggctc tagctttggc 16167
aagtttttaa cactgatttt ctggtttttt tttttttttg cagaattttt cagagatagg 16227
gggctcattc cagcagggtt tcccactata tttcgcattt tttccaaaaa tttttgtatt 16287
ttcaaaaatt tccaaaaaga aaggggtttt ctttaccaaa tttttctcgc cacttttggc 16347
ttaattttgg ctttagagat tcgatcgaaa aaattgcgaa agtggcgaga aatctcactg 16407
gtttgatgtt tgaccccta ctatagaaaa tttgaaaaaa aaaaaaaaaa aaaaaaacta 16467
gacgaaattt gtggaaatct tgctggagtt tgacgagtcg atggtggatt tttcttgaaa 16527
cgaatgaaac ggtgattttg gatcggagaa atatggcgaa aaatggtgag aaatgacgag 16587
gaggaggaag aagctgaaaa tctggaggaa caaaaattgt gtggaagtct cgggaagaaa 16647
ttagaattga aattttaaag tgttctgaga attttttgtg tgaaattttt ttaaatctgt 16707
agatcaaata tcaaaaaaaa aaatcagaac tattacgtgt ttatccacaa agatgagaaa 16767
aatcgccata tctggcgcgc aaatgaaccc gcgggaagag acaaaactac tgtagttttt 16827
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aaaaaatttt ttttaaaaat tgcggctcaa aattaaattc aattcgatga cgcaatagct 17007
cgtaaatcta cacaaattgg ttaaaaacta cagtagtttt gtctcttccc gcgggttcat 17067
ttgcgcgcca gatatggtga ttttctcat ctctggataa acacgtaata acatttctcg 17127
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ggctacaata tttagtagaa agtgataaat aaataaaaat taggttccag acgttgcgac 17727
accgagaagt tggcgaaaac tttgatttta gctaaaaata agccatttc ccaaaacttt 17787
gagcggtcat aacttttttt tgagaaagaa attttcagaa tgtctcatta cgaaattcgg 17847
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gcctttacct tggtgaaatt ttttaatctg tagtatactt tatttttggc cgacttttg 17967
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aattttgtc ggttttcttc gcgccaaaaa gtacggtaac aggtttcggc acgatacatt 18087
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gaaattttga ttttcggcaa tataccgatt tgccggaaca tttggtttcc ggcaatatgc 18627
cgatttgccg gaatttttgg ttttcggaaa tttccggaa atttagaatt ccggcaattt 18687
gccgatttgc cggaaatttt gatttccggc aatatgccga tttgccggaa attttggttt 18747
tcggaaattt gccggaaatt tagaattccg gcaatatgcc gatttgccgg aaattttgat 18807
ttccggcaat atgccgattt gtcagaagaa atcgtttgtc acccacacgt gtattgattt 18867
gattttct ag ata aaa ttc tac gac gag ctg gac gat atc atg cca atc 18917
            Glu Ile Lys Phe Tyr Asp Glu Leu Asp Asp Ile Met Pro Ile
                      1515              1520


tgg ctt cca cca tca cca cca gat tcg gat gcg gat ttc gac ttg aga   18965
Trp Leu Pro Pro Ser Pro Pro Asp Ser Asp Ala Asp Phe Asp Leu Arg
1525            1530              1535              1540
```

Fig. 19L

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```
atg gaa gat gat tgt ctc gat ctg atg tat gaa att gaa caa atg aac   19013
Met Glu Asp Asp Cys Leu Asp Leu Met Tyr Glu Ile Glu Gln Met Asn
            1545                1550                1555

gag gct cgc cta cca caa gtt tgt cat gaa atg aga cgt ccg ttg gct   19061
Glu Ala Arg Leu Pro Gln Val Cys His Glu Met Arg Arg Pro Leu Ala
            1560                1565                1570

gaa aaa cag cag aaa cag aac acg ttg aat gcg ttt aa tggtaatatt    19109
Glu Lys Gln Gln Lys Gln Asn Thr Leu Asn Ala Phe Lys
            1575                1580                1585

ttcaaaaaaa aattttttg aaaaaattca attaaattcg attttgagca atttttatcg 19169
tgaagattgc ataattttga gattttgcgc caagattttt gttaaattga aaaaaagaga 19229
tgtgcgcctt tatggagtac tgtagttttg aaaattgaaa ttacagtact ctgtttaaag 19289
gcgcacacat gtattacgta gcgaaaagaa aagtacagta attagttaaa taagactact 19349
gtagcgcttg tgtcgattta cgggctctga attttatatg aatttttgaa aactagaaac 19409
atctcaaatt gcataaaatt accatttgaa cctcccgcca agtgattttg ttcgacgggg 19469
cgcgcttgca cgttttctat tttaatttaa ttcaattttt tttgcttaat tctcaccgat 19529
ttttcatgtt ttcagtttga ttttgatgga aatttggaga caatatcaac ataaatgctt 19589
ttcaatcgaa aatgtgcatt tatattgaca ttttctccga atttccatca aaattaaact 19649
gaaaacacga aaaatcggtg agaattaagc gaaaaaattg agttaaatga aaatagaaaa 19709
cgtgcaagcg cgctccatcg aacaaaatca attggcggga ggttcaaatg ggaattgtat 19769
gcaattttca aaaggtcgta taaaattttg aagaaagcaa attaaattta aaaaatcgag 19829
ctcgtaaatc gacacaggcg ctaattttca aaaaaataaa atgacaccca aaaaatcata 19889
agaaaatcat aaataaatat tacgggaaca caaaactcag agaacccgta ttgcacaaca 19949
tatttgacgc gcaaaatatg aaatatctcg tagcgaaaag aaaactaccg taatttaaaa 20009
acatttaaat gactactgta gcgcttgtgt cgatttacga gatctcgatt ttctaaataa 20069
attttttaaa aaatgatgtc agcgatattc catttgactt tgtttcttcg tattattttc 20129
tcatttttgc ttgattttat ttaattttat aatttttattt aaaatcaagc aaaaacgaga 20189
aaataatacg aagaaacgga gttaaatgga atatcgctga cataatttaa aaaaaaaatt 20249
taattagaaa atcgagatcc cgtaaatcga cacaagtagt catagtacag tagtcattta 20309
actaattact gtactttttct tttcgctgcg agatatttca tattttttatt catattttta 20369
tttattttca tatttttata tatatatata tatatatatt tcttggcgtt ctaatgcagt 20429
ttctctcaat taattcc a gac att cta tcg gca aaa gaa aag gaa tcg gtg 20480
                 Asp Ile Leu Ser Ala Lys Glu Lys Glu Ser Val
                         1590                1595

tac gat gcg gtc aac aag tgc ctt caa atg cca caa tcc gaa gcg atc   20528
Tyr Asp Ala Val Asn Lys Cys Leu Gln Met Pro Gln Ser Glu Ala Ile
            1600                1605                1610

aca gca gaa tct gca gcg tct cca gca tac acg gaa cac tca tca ttc   20576
Thr Ala Glu Ser Ala Ala Ser Pro Ala Tyr Thr Glu His Ser Ser Phe
            1615                1620                1625

tcg atg gat gat aca agc cag gat gcg aag att gag cca agt ttg act   20624
Ser Met Asp Asp Thr Ser Gln Asp Ala Lys Ile Glu Pro Ser Leu Thr
            1630                1635                1640

gaa aat caa caa ccc acc acc acc gcc act act act act aca gta ccc   20672
Glu Asn Gln Gln Pro Thr Thr Thr Ala Thr Thr Thr Thr Thr Val Pro
1645                1650                1655                1660
```

Fig. 19M

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```
caa caa caa caa caa cag cag cag caa aaa tcg tcg aaa aag aag aga   20720
Gln Gln Gln Gln Gln Gln Gln Gln Gln Lys Ser Ser Lys Lys Lys Arg
            1665                1670                1675


aat gat aat cga a cggtacggag gttactagcg aacaatttca agaaattttg   20773
Asn Asp Asn Arg
            1680


aatttgtgaa aattcaattc cggcaatttt tcgatttgcc ggaactttta attttcgccg 20833
aattgtcaat ttgccggaaa ttttgatttc cgccgaattg tcgatttgcc ggaacttttc 20893
attttcggca aattttcgat ttgccggaac ttttaatttt tgacaaattg tcgatgtgcc 20953
ggaaattttg attttcgaca atttgctgat ttgccggaaa tttcaatccc aacaattttc 21013
cgatttgccg gaaatttcaa tcccaacaat tttccgattt gccggaaatt tcaatcccaa 21073
caattttccg atttgccgga aatttcaatc ccaacaattt tccgatttgc cggaaatttc 21133
aatcccagca attttccgat ttgccggaaa tttcaattcc ggcaattttt cgatttgccg 21193
gaacttttca ttttcggcaa agtgtcgatt tgccggaact tttcattttc gccgaattgt 21253
cgatttgccc gaactttaa tttttgacaa attgtcgttt tgctggaaat tttgattttc 21313
gacaatttgc caatttgccg gaactttaa tttttgacaa attgtcgatt tgccggaaat 21373
tttgattttc gacaatttgc caatttgccg gaacttttca ttttgccaa attgtcgatt 21433
tgccggaaat tttaattccg gcaattttgc gatttgccgg aaatttcaat tccggcaatt 21493
taaaaacact aaaaaccaaa aattttcggt tttcccgttt ttcgatgttt cagcttttct 21553
caaaaaattg cgattccccg aaaaatcgaa acaattttcg gggttaaaac cgggaaattc 21613
ctaaattcct atttaaaaga attgaaaaaa aactctcaaa attcc ag gct caa aat 21669
                                                   Lys Ala Gln Asn


cga aca gct gaa aat ggt gtg aaa cga gcg aca act cca cca cca tca   21717
Arg Thr Ala Glu Asn Gly Val Lys Arg Ala Thr Thr Pro Pro Pro Ser
1685                1690                1695                1700


tgg cgt gaa gag cca gat tat gat gga gcc gaa tgg aat ata gtt gaa   21765
Trp Arg Glu Glu Pro Asp Tyr Asp Gly Ala Glu Trp Asn Ile Val Glu
                    1705                1710                1715


gat tat gca cta ctt caa gca gtt caa gtc gaa ttt gca aat gct cat   21813
Asp Tyr Ala Leu Leu Gln Ala Val Gln Val Glu Phe Ala Asn Ala His
                1720                1725                1730


tta gtc gaa aaa tcg gcg aat gag gga atg gtg ttg aac tgg gaa ttc   21861
Leu Val Glu Lys Ser Ala Asn Glu Gly Met Val Leu Asn Trp Glu Phe
            1735                1740                1745


gtg tcg aat gcc gtt aat aag cag aca aga ttt ttc cgc tcg gcc cgt   21909
Val Ser Asn Ala Val Asn Lys Gln Thr Arg Phe Phe Arg Ser Ala Arg
        1750                1755                1760


caa tgc tca att cga tat caa atg ttt gtt cgg cca aaa gag ctc gga   21957
Gln Cys Ser Ile Arg Tyr Gln Met Phe Val Arg Pro Lys Glu Leu Gly
1765                1770                1775                1780


cag ttg gtg gct tct gat ccg att tcc aag aaa acg atg aaa gtc gac   22005
Gln Leu Val Ala Ser Asp Pro Ile Ser Lys Lys Thr Met Lys Val Asp
                1785                1790                1795


cta tcg cat act gaa tta tct cat ttg aga aaa gga cga atg act acg   22053
Leu Ser His Thr Glu Leu Ser His Leu Arg Lys Gly Arg Met Thr Thr
                1800                1805                1810
```

Fig. 19N

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```
gag agc caa tat gct cat gat tat gga ata ttg act gat aag aaa cat    22101
Glu Ser Gln Tyr Ala His Asp Tyr Gly Ile Leu Thr Asp Lys Lys His
        1815            1820            1825

gtg aat aga ttt aaa agt gtt cga gtg gcg gca aca cgg aga cct gtt    22149
Val Asn Arg Phe Lys Ser Val Arg Val Ala Ala Thr Arg Arg Pro Val
        1830            1835            1840

cag ttt tgg aga ggc cct aaa ggt aga gga gga tgg ctt cat aat agt    22197
Gln Phe Trp Arg Gly Pro Lys Gly Arg Gly Gly Trp Leu His Asn Ser
1845            1850            1855            1860

cac tgc aac ttt ttc ctc acg agg gac gag aaa aag tgg ttt cta ggc    22245
His Cys Asn Phe Phe Leu Thr Arg Asp Glu Lys Lys Trp Phe Leu Gly
            1865            1870            1875

cat ggc cga ggt gcc gac aag ttt ca gcggccattt atcttgcttt          22291
His Gly Arg Gly Ala Asp Lys Phe
            1880
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Fig. 19O

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Fig. 19P

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Fig. 19Q

Title: RB PATHWAY AND CHROMATIN REMODELING
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Fig. 19R

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tggtctatta atagatctcc aaggatatac atacatgtat ctgatagttt gctcattgat 35611
tcaaatgtgc aataaaatga cgcatccaat ggaccaggat ctttgcaaag tttcgcttca 35671
atgttttcag tagaaattcc aaggttcaat agggcaacta tctcagtaat ggtgacacaa 35731
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tttcgttttg atcttcaaaa aatgcgggag ttcagaccta gacatctcgt ctgatttcgc 36571
atggttaaga gcgttctgac gtcacaattt ttctgaaaaa atattcccgc atttttttgta 36631
gatcaaatta aaatgagaca gcctgacacc acgtggagtt ccttatatac aaaaaagttg 36691
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acattaaagt ttccttttttc tttgtcagct gtaaaaaccg aaaggcttgt cagactagta 36991
ttctcaatat taaatc                                                 37007
```

Fig. 19S

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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lin-65 genomic sequence (1 kb of upstream and downstream
genomic sequence is included in this file)

Exon number	Exon boundaries (inclusive)
1	1001 - 1133
2	4522 - 5208
3	6128 - 6361
4	7962 - 8350
5	8706 - 8928
6	9260 - 9516
7	10328 - 10567
8	11677 - 11700

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TTTGCAAAAAAAAAATTCAAAAACCGCATTTTTCTCAGAATTTTTCTGGGATTTTG
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Fig. 27A

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GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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CTAGGCCACCAAAAATGTTTCTAGGCCACCAAAAAGGTTTCTAGGCCACCAAAC
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Fig. 27B

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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```
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Fig. 27C

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
Filing Date: September 12, 2003
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```

Fig. 27D

Title: RB PATHWAY AND CHROMATIN REMODELING
GENES THAT ANTAGONIZE *LET-60* RAS SIGNALING
Applicant(s):Horvitz *et al.*
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Fig. 27E

Title: RB PATHWAY AND CHROMATIN REMODELING
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Applicant(s):Horvitz *et al.*
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Fig. 27F